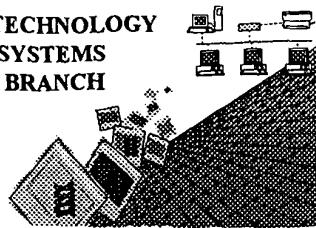


re-run

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/697,863
Source: 1600
Date Processed by STIC: 11/13/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/697,863

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/697,863¹ DATE: 11/13/2000
 TIME: 17:30:41

Input Set : A:\sequence listing.txt
 Output Set: N:\CRF3\11132000\I697863.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
 5 <120> TITLE OF INVENTION: CD40-INTERACTING AND TRAF-INTERACTING PROTEINS
 7 <130> FILE REFERENCE: V7/002-V018
 9 <140> CURRENT APPLICATION NUMBER: US/09/697,863
 10 <141> CURRENT FILING DATE: 2000-10-27
 12 <150> PRIOR APPLICATION NUMBER: 98201392.2
 13 <151> PRIOR FILING DATE: 1998-04-29
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1920
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (20)..(1108)
 28 <400> SEQUENCE: 1
 29 gtgcagagggc ggcaggaag atg gag ttg ggg agt tgc ctg gag ggc ggg agg 52
 30 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg
 31 1 5 10
 33 gag gcg gcg gag gaa gag ggc gag cct gag gtg aaa aag cgg cga ctt 100
 34 Glu Ala Ala Glu Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu
 35 15 20 25
 37 ctg tgt gtg gag ttt gcc tcg gtc gca agc tgc gat gcc gca gtg gct 148
 38 Leu Cys Val Glu Phe Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala
 39 30 35 40
 41 cag tgc ttc ctg gcc gag aac gac tgg gag atg gaa agg gct ctg aac 196
 42 Gln Cys Phe Leu Ala Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn
 43 45 50 55
 45 tcc tac ttc gag cct ccg gtg gag gag agc gcc ttg gaa cgc cga cct 244
 46 Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro
 47 60 65 70 75
 49 gaa acc atc tct gag ccc aag acc tat gtt gac cta acc aat gaa gaa 292
 50 Glu Thr Ile Ser Glu Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu
 51 80 85 90
 53 aca act gat tcc acc act tct aaa atc agc cca tct gaa gat act cag 340
 54 Thr Thr Asp Ser Thr Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Glu
 55 95 100 105
 57 caa gaa aat ggc agc atg ttc tct ctc att acc tgg aat att gat gga 388
 58 Gln Glu Asn Gly Ser Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly
 59 110 115 120
 61 tta gat cta aac aat ctg tca gag agg gct cga ggg gtg tgt tcc tac 436
 62 Leu Asp Leu Asn Asn Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr
 63 125 130 135
 65 tta gct ttg tac agc cca gat gtg ala ttt cta cag gaa gtt att ccc 484
 66 Leu Ala Leu Tyr Ser Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro
 67 140 145 150 155

pp 2-3

see P. 5, two

RAW SEQUENCE LISTING

DATE: 11/13/2000

PATENT APPLICATION: US/09/697,863

TIME: 17:30:41

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\11132000\I697863.raw

```

69 cca tat tat agc tac cta aag aag aga tca agt aat tat gag att att 532
70 Pro Tyr Tyr Ser Tyr Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile
71                               160                               165                               170
73 aca ggt cat gaa gaa gga tat ttc aca gct ata atg ttg aag aaa tca 580
74 Thr Gly His Glu Glu Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser
75                               175                               180                               185
77 aqa gtg aaa tta aaa agc caa gag att att cct ttt cca agt acc aaa 628
78 Arg Val Lys Leu Lys Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys
79                               190                               195                               200
81 atg atg aga aac ctt tta tgt gtg cat gtg aat gtg tca gga aat gag 676
82 Met Met Arg Asn Leu Leu Cys Val His Val Asn Val Ser Gly Asn Glu
83                               205                               210                               215
85 ctt tgc ctt atg aca tcc cat ttg gag agc acc aga ggg cat gct gcg 724
86 Leu Cys Leu Met Thr Ser His Leu Glu Ser Thr Arg Gly His Ala Ala
87 220                               225                               230                               235
89 gaa cga atg aat cag tta aaa atg gtt tta aag aaa atg caa gag gct 772
90 Glu Arg Met Asn Gln Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala
91                               240                               245                               250
93 cca gag tca gct aca gtt ata ttt gca gga gat aca aat cta agg gat 820
94 Pro Glu Ser Ala Thr Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp
95                               255                               260                               265
97 cga gag gtt acc aga tgt ggt ggt tta ccc aac aac att gtg gat gtc 868
98 Arg Glu Val Thr Arg Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val
99                               270                               275                               280
101 tgg gag ttt ttg ggc aaa cct aaa cat tgc cag tat aca tgg gat aca 916
102 Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr
103                               285                               290                               295
105 caa atg aac tct aat ctt gga ata act gct gct tgt aaa ctt cgt ttt 964
106 Gln Met Asn Ser Asn Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe
107 300                               305                               310                               315
109 gat cga ata ttt ttc aga gca gca gca gaa gag gga cac att att ccc 1012
110 Asp Arg Ile Phe Phe Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro
111                               320                               325                               330
113 cga agt ttg gac ctt ctt gga tta gaa aaa ctg gac tgt ggt aga ttt 1060
114 Arg Ser Leu Asp Leu Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe
115                               335                               340                               345
117 cct aat gat cac tgg ggt ctt ctg tgc aac tta gat ata ata ttg taa 1108
118 Pro Ser Asp His Trp Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
119                               350                               355                               360
121 aatgcttttc aagtgtgggt ttgtccctga ttgttgcaaa tacaatttcc accttctgga 1168
123 aaggtagggt tgcgtgagg gaaataatgt actagatcat tgtcacagaa aaaccaacta 1228
125 tgatttatgg ttgtgttttc agaattcaac attaaagatt aatgtttatt taaacgaaca 1288
127 cattcctgca ttcaggatgt gaggccatit aataaaaagg gcacaaaagcc tgtcagagtt 1348
129 ttcaacgggtg cttacagctg ccagctggat tccaaacagg taccceattg tctctgagct 1408
131 aatgtttata tttttccatt caggcaccga aatagttaat attttaaata agtcttcaaa 1468
133 agaaaacata agagattatt gagttcttgg gactggatcc ttattttcat aagttcagat 1528
135 catcttaaat gaaaatgccg tgattatctg cagttaagta gatgacagct attctacatc 1588
W--> 137 agacttgatt ttgtcagct aattacataa ttggttaag ataattgaaa ccttatggct 1648
139 taaaattcct taactccttt ttgattcatg ttgttagtca tgttgtaaac agaggcaaaag 1708

```

→ see item 10 on
Erra Summary
sheet

RAW SEQUENCE LISTING

DATE: 11/13/2000

PATENT APPLICATION: US/09/697,863

TIME: 17:30:41

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\11132000\I697863.raw

141 ttaagcttga tgatgggttaa aatcggtttg atagcaccat gggacatttt ttttaacaaaa 1768
 143 ataaatgcat gaagagacat agccttttag ttttgctaatt tgtgaaatgg aaatgcttta 1828
 W--> 145 caggaagtaa atgcaaatta **0**ttttaagtg tgcttttaaag aaaaatattt tccccacagg 1888
 147 agaaatttaa ataaagaatt ctatttggtta aa 1920
 150 <210> SEQ ID NO: 2
 151 <211> LENGTH: 362
 152 <212> TYPE: PRT
 153 <213> ORGANISM: Homo sapiens
 155 <400> SEQUENCE: 2
 156 Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
 157 1 5 10 15
 159 Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
 160 20 25 30
 162 Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
 163 35 40 45
 165 Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
 166 50 55 60
 168 Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
 169 65 70 75 80
 171 Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
 172 85 90 95
 174 Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
 175 100 105 110
 177 Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
 178 115 120 125
 180 Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
 181 130 135 140
 183 Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
 184 145 150 155 160
 186 Leu Lys Lys Arg Ser Ser Asn Tyr Glu Ile Ile Thr Gly His Glu Glu
 187 165 170 175
 189 Gly Tyr Phe Thr Ala Ile Met Leu Lys Lys Ser Arg Val Lys Leu Lys
 190 180 185 190
 192 Ser Gln Glu Ile Ile Pro Phe Pro Ser Thr Lys Met Met Arg Asn Leu
 193 195 200 205
 195 Leu Cys Val His Val Asn Val Ser Gly Asn Glu Leu Cys Leu Met Thr
 196 210 215 220
 198 Ser His Leu Glu Ser Thr Arg Gly His Ala Ala Glu Arg Met Asn Gln
 199 225 230 235 240
 201 Leu Lys Met Val Leu Lys Lys Met Gln Glu Ala Pro Glu Ser Ala Thr
 202 245 250 255
 204 Val Ile Phe Ala Gly Asp Thr Asn Leu Arg Asp Arg Glu Val Thr Arg
 205 260 265 270
 207 Cys Gly Gly Leu Pro Asn Asn Ile Val Asp Val Trp Glu Phe Leu Gly
 208 275 280 285
 210 Lys Pro Lys His Cys Gln Tyr Thr Trp Asp Thr Gln Met Asn Ser Asn
 211 290 295 300
 213 Leu Gly Ile Thr Ala Ala Cys Lys Leu Arg Phe Asp Arg Ile Phe Phe
 214 305 310 315 320

12
 10

RAW SEQUENCE LISTING DATE: 11/13/2000
 PATENT APPLICATION: US/09/697,863 TIME: 17:30:41

Input Set : A:\sequence listing.txt
 Output Set: N:\CRF3\11132000\I697863.raw

```

216 Arg Ala Ala Ala Glu Glu Gly His Ile Ile Pro Arg Ser Leu Asp Leu
217                               325                               330                               335
219 Leu Gly Leu Glu Lys Leu Asp Cys Gly Arg Phe Pro Ser Asp His Trp
220                               340                               345                               350
222 Gly Leu Leu Cys Asn Leu Asp Ile Ile Leu
223                               355                               360
227 <210> SEQ ID NO: 3
228 <211> LENGTH: 1312
229 <212> TYPE: DNA
230 <213> ORGANISM: Mus musculus
232 <220> FEATURE:
233 <221> NAME/KEY: CDS
234 <222> LOCATION: (122)..(1234)
236 <400> SEQUENCE: 3
237 agctattaat gattcgaaatt tatacgactc actatagggg atttggccct cgaggccaag 60
238 aattcggcac qagggcggga agcagcgtga agacgggtg ttttgaggga accctgcggc 120
241 g atg gcg tct gcc agc agt tcc gat gcg gcg gag ccc gca ggg ccg gca 169
242 Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
243 1 5 10 15
245 ggg cgg gcg gcg tgg gcg ccc gaa gca gca cag gcg gag gag gac cgg 217
246 Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
247 20 25 30
249 gtg aag agg cgg cgg ctt cag tgc ctg gcc ttt gcg ttg gtg ggg gga 265
250 Val Lys Arg Arg Arg Leu Gln Cys Leu Gly Phe Ala Leu Val Gly Gly
251 35 40 45
253 tgc gac ccc acg atg gtc ccc agc gtc ctg cgg gag aac gac tgg cag 313
254 Cys Asp Pro Thr Met Val Pro Ser Val Leu Arg Glu Asn Asp Trp Gln
255 50 55 60
257 acg cag aaa gcc ctg agc gcc tac ttc gag ctg cca gag aac gac caa 361
258 Thr Gln Lys Ala Leu Ser Ala Tyr Phe Glu Leu Pro Glu Asn Asp Gln
259 65 70 75 80
261 ggg tgg ccg cgc cag cct ccc acg tcc ttc aag tcc gag gcc tat gtt 409
262 Gly Trp Pro Arg Gln Pro Pro Thr Ser Phe Lys Ser Glu Ala Tyr Val
263 85 90 95
265 gat cta acc aac gag gat gca aat gat aca acc att tta gaa gcc agt 457
266 Asp Leu Thr Asn Glu Asp Ala Asn Asp Thr Thr Ile Leu Glu Ala Ser
267 100 105 110
269 cca tct gga act cct cta gaa gat agc agc act att tct ttc att acc 505
270 Pro Ser Gly Thr Pro Leu Glu Asp Ser Ser Thr Ile Ser Phe Ile Thr
271 115 120 125
273 tgg aat att gat gga tta gat gga tgc aat ctg ccc gag agg gct cga 553
274 Trp Asn Ile Asp Gly Leu Asp Gly Cys Asn Leu Pro Glu Arg Ala Arg
275 130 135 140
277 ggg gtg tgt tcc tgc cta gct ttg tat agt cca gat gtg gta ttt cta 601
278 Gly Val Cys Ser Cys Leu Ala Leu Tyr Ser Pro Asp Val Val Phe Leu
279 145 150 155 160
281 cag gaa gtt atc ccc cca tac tgt gcc tac cta aag aag aga gca gcc 649
282 Gln Glu Val Ile Pro Pro Tyr Cys Ala Tyr Leu Lys Lys Arg Ala Ala
283 165 170 175

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,863

DATE: 11/13/2000

TIME: 17:30:41

Input Set : A:\sequence_listing.txt

Output Set: N:\CRF3\11132000\I697863.raw

```

285 agt tac aca att att aca ggt aat gaa gaa gga tat ttc aca gct ata 697
286 Ser Tyr Thr Ile Ile Thr Gly Asn Glu Glu Gly Tyr Phe Thr Ala Ile
287      180      185      190
289 cta ttg aag aaa gga aga gtg aaa ttt aaa agt cag gag att att cct 745
290 Leu Leu Lys Lys Gly Arg Val Lys Phe Lys Ser Gln Glu Ile Ile Pro
291      195      200      205
293 ttt cca aat acc aaa atg atg aga aac ctg cta tgc gta aat gtg agt 793
294 Phe Pro Asn Thr Lys Met Met Arg Asn Leu Leu Cys Val Asn Val Ser
295      210      215      220
297 ttg ggt gga aat gaa ttt tgc ctt atg aca tcc cat ttg gag agc acc 841
298 Leu Gly Gly Asn Glu Phe Cys Leu Met Thr Ser His Leu Glu Ser Thr
299 225      230      235      240
301 aga gaa cat tct gcg gaa cga ata aqa caa tta aaa act gtt ctt gga 889
302 Arg Glu His Ser Ala Glu Arg Ile Arg Gln Leu Lys Thr Val Leu Gly
303      245      250      255
305 aaa atg caa gag gct cca gat tca acc acg gtt ata ttt gca gga gat 937
306 Lys Met Gln Glu Ala Pro Asp Ser Thr Thr Val Ile Phe Ala Gly Asp
307      260      265      270
309 aca aat tta aga gat caa gaa qtt atc aaa tgt ggt ggt tta cct gac 985
310 Thr Asn Leu Arg Asp Gln Glu Val Ile Lys Cys Gly Gly Leu Pro Asp
311      275      280      285
313 aac gtt ttt gat gcc tgg gaa ttt tta ggc aaa cct aaa cat tgc cag 1033
314 Asn Val Phe Asp Ala Trp Glu Phe Leu Gly Lys Pro Lys His Cys Gln
315      290      295      300
317 tat aca tgg gat acg aaa gca aat aac aac ctc agg atc cct gct gct 1081
318 Tyr Thr Trp Asp Thr Lys Ala Asn Asn Asn Leu Arg Ile Pro Ala Ala
319 305      310      315      320
321 tat aag cat cgt ttt gat cga ata ttt ttc aga gca gaa gag qgg cac 1129
322 Tyr Lys His Arg Phe Asp Arg Ile Phe Phe Arg Ala Glu Glu Gly His
323      325      330      335
325 ctt att cct caa agt tta gac ctt gtt ggg ttg gaa aaa ctg gac tgt 1177
326 Leu Ile Pro Gln Ser Leu Asp Leu Val Gly Leu Glu Lys Leu Asp Cys
327      340      345      350
329 ggt aga ttt ccg agt gat cac tgg ggg ctc ttg tgc acc ttg aat gta 1225
330 Gly Arg Phe Pro Ser Asp His Trp Gly Leu Cys Thr Leu Asn Val
331      355      360      365
333 gta ttg tga aaagcttccc acttgcagct ttacacgttt gttatgacta 1274
334 Val Leu
335      370
337 gttctgaatt tgtgtaggtc tcaaccttcc aggacatc 1312
340 <210> SEQ ID NO: 4
341 <211> LENGTH: 370
342 <212> TYPE: PRT
343 <213> ORGANISM: Mus musculus
345 <400> SEQUENCE: 4
346 Met Ala Ser Gly Ser Ser Ser Asp Ala Ala Glu Pro Ala Gly Pro Ala
347 1      5      10      15
349 Gly Arg Ala Ala Ser Ala Pro Glu Ala Ala Gln Ala Glu Glu Asp Arg
350      20      25      30

```

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 11/13/2000
PATENT APPLICATION: US/09/697,863 TIME: 17:30:42

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\11132000\I697863.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:137 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:137 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:145 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:536 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:536 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:537 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:548 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:549 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:630 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:630 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:630 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:630 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:630 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:639 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6